Allelic Loss in Esophageal Sequamous Cell Carcinoma Patients with and without Family History of Upper Gastrointestinal Tract Cancer

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Abstract: Chromosomal regions with frequent allelic loss may point to major susceptibility genes that will assist in under-standing molecular events involved in esophageal carcinogenesis. Esophageal squamous cell carcinoma samples and blood from 46 patients, including 23 patients with and 23 patients without a family history of upper gastrointestinal cancer, were screened using laser microdissected DNA and tested for loss of heterozygosity (LOH) at 18 marker loci representing 14 chromosomal regions (on 2q, 3p, 4p, 4p, 5q, 6q, 8p, 9p, 9q, 11p, 13q, 14q, 15q, and 17p) identified in an earlier genome-wide scan to have frequent LOH. Clinical/pathological and lifestyle risk factor data were also collected. For all 46 tumors combined, the lowest frequency LOH for any of the 18 markers was 37%, and 8 markers showed LOH in $\geq$75 % of infornnative tumors. One marker (D13S894 on 13q) showed greater LOH in patients with a positive family history (93% Venus 50%; P = 0.04), whereas two markers (D6S1027 on 6q and D9S910 on 9q) had significantly more LOH in patients with metastasis, and one marker (D4S2361 on 4p) showed significantly higher LOH in patients with a lower pathological tumor grade. No relation was seen between LOH and lifestyle risk factors. This study confirms the previously observed high frequency LOH for these 14 chromosomal regions, including a locus on 13q where LOH is more common in patients with a family history of upper gastrointestinal cancer than in those with-out such history, suggesting that a gene in this area may be involved in genetic susceptibility to esophageal cancer.